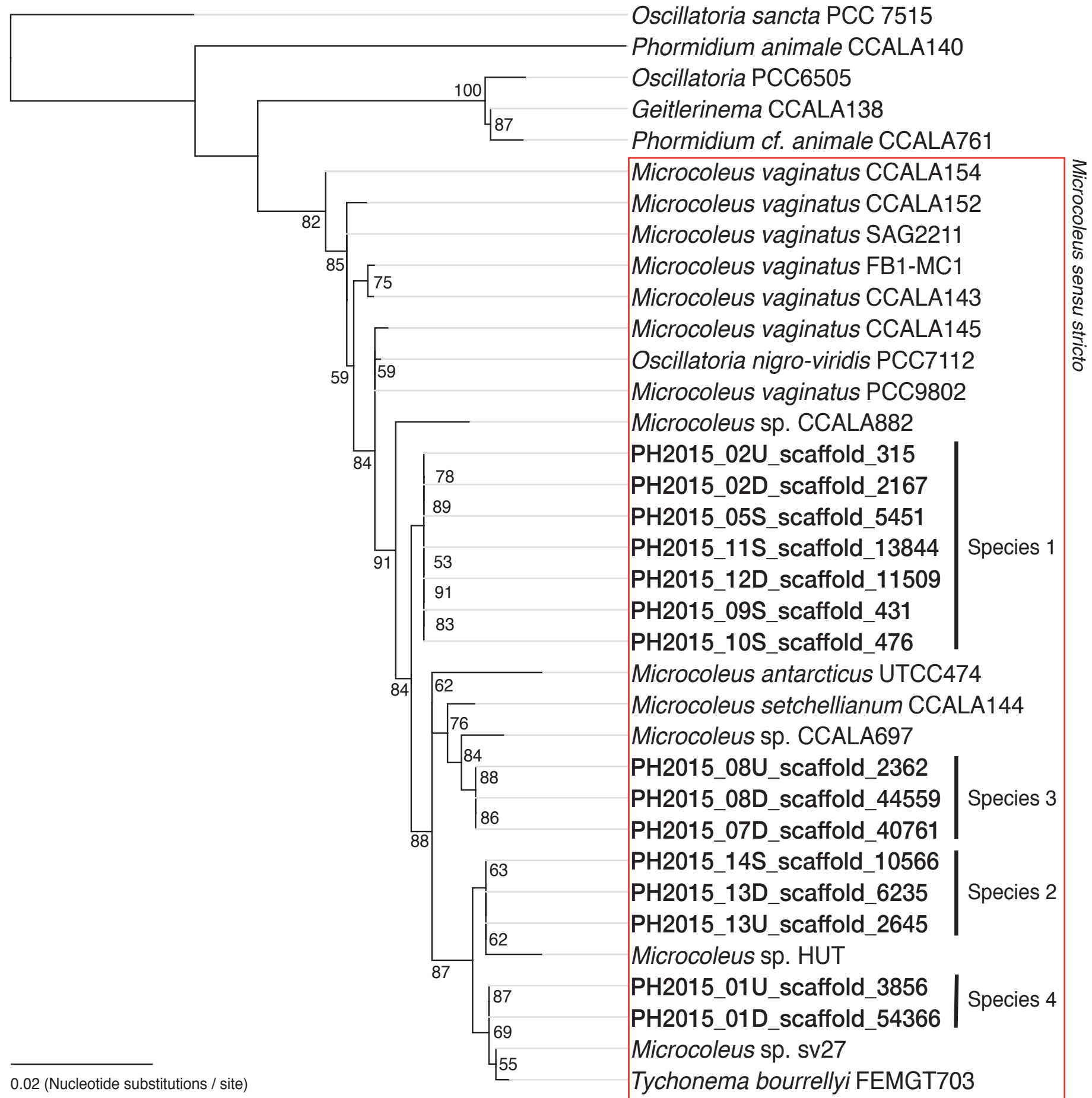
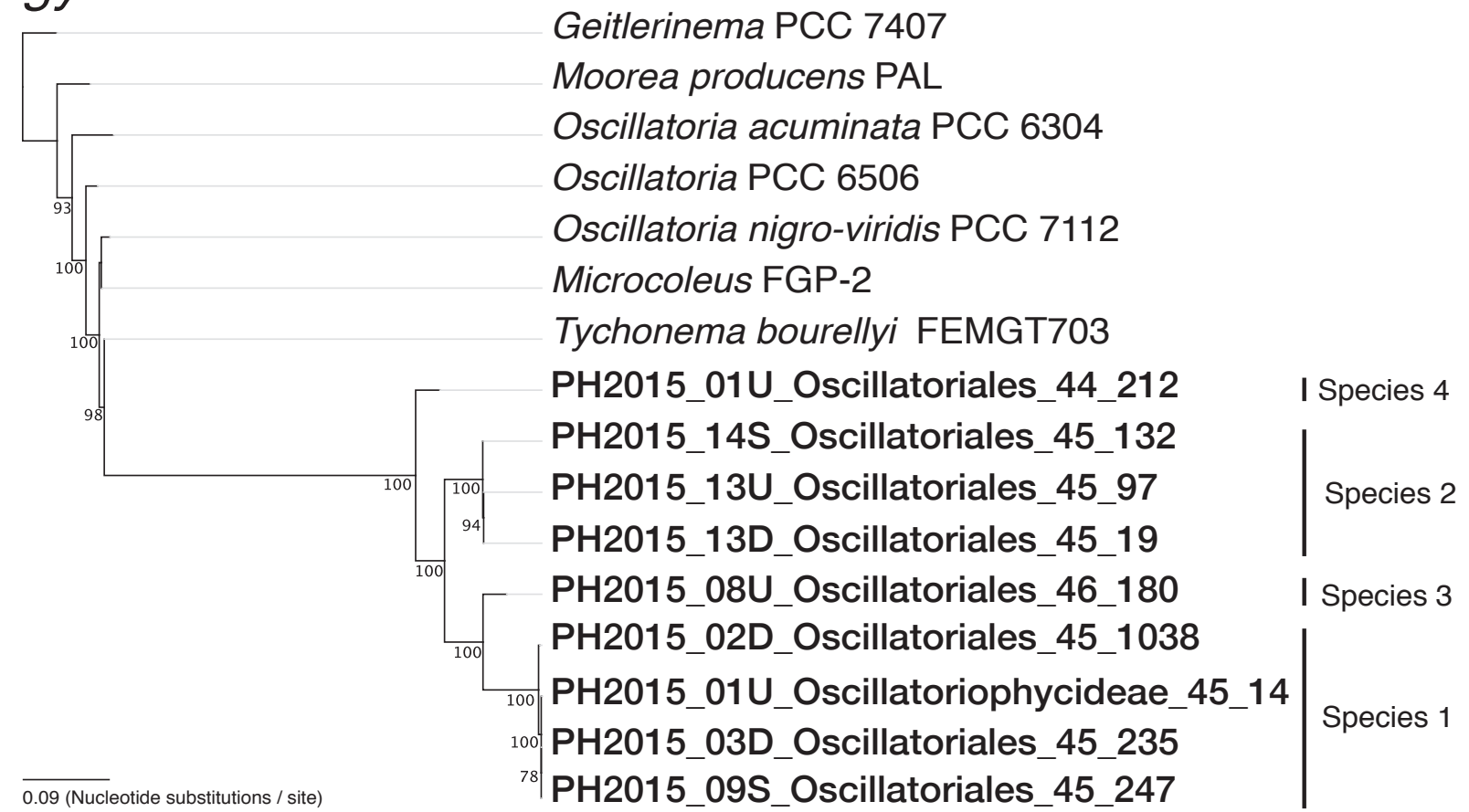


16S rRNA



gyrB



rbcL

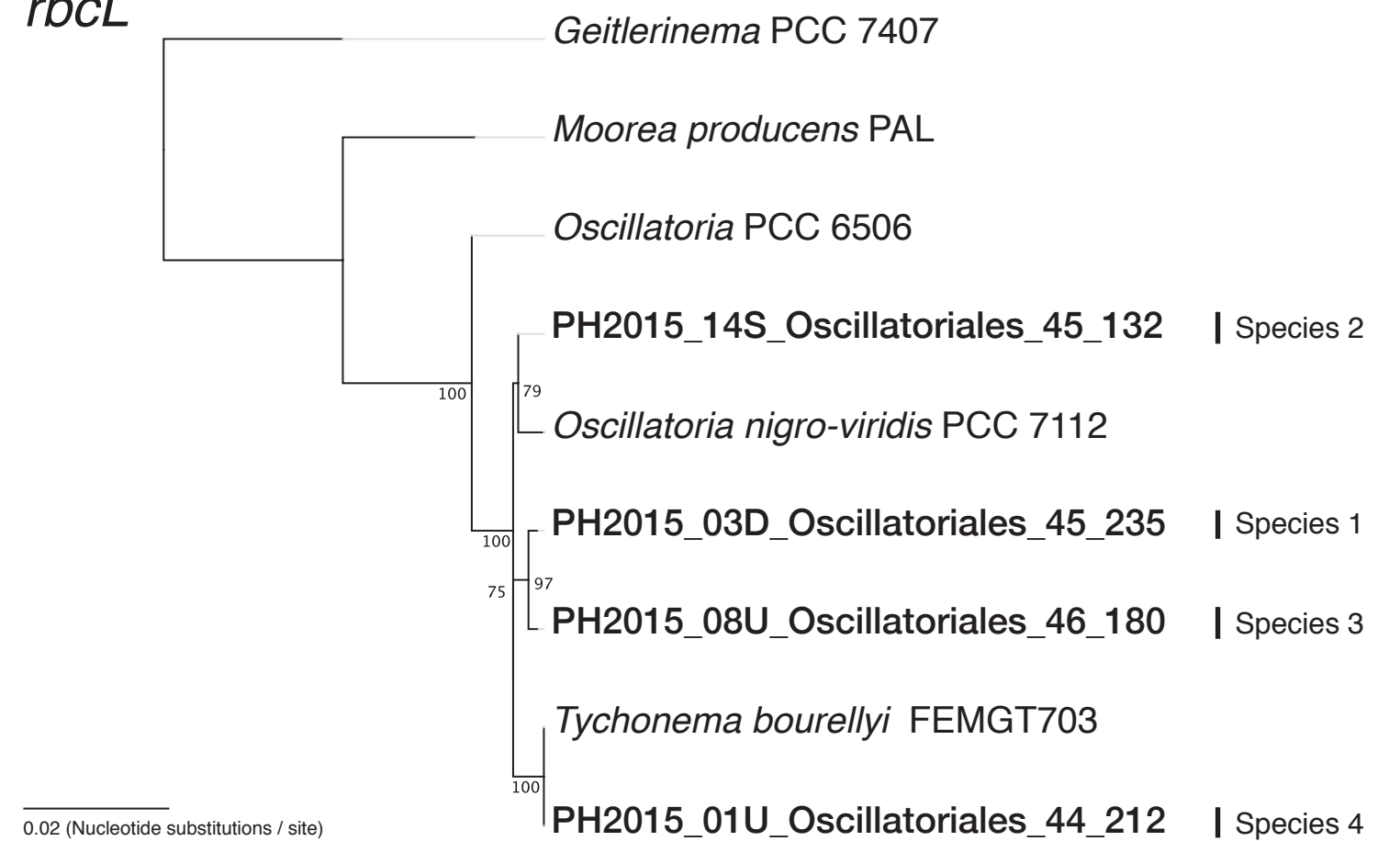


Figure S3 Maximum likelihood trees of nucleotide sequences from the 16S rRNA, *gyrB*, and *rbcL* genes. Sample sequences are in bold, and accession numbers for reference strains can be found in Table S2. The species identity of sample strains (determined by average nucleotide identity, see Figure 3 in text) is indicated on the right side of each tree. Each tree was bootstrapped 100 times and, bootstrap support is shown for nodes with support >50,. The *Microcoleus sensu stricto* clade is shown in red on the 16S rRNA tree, as was defined by Strunecký et al. (2013).